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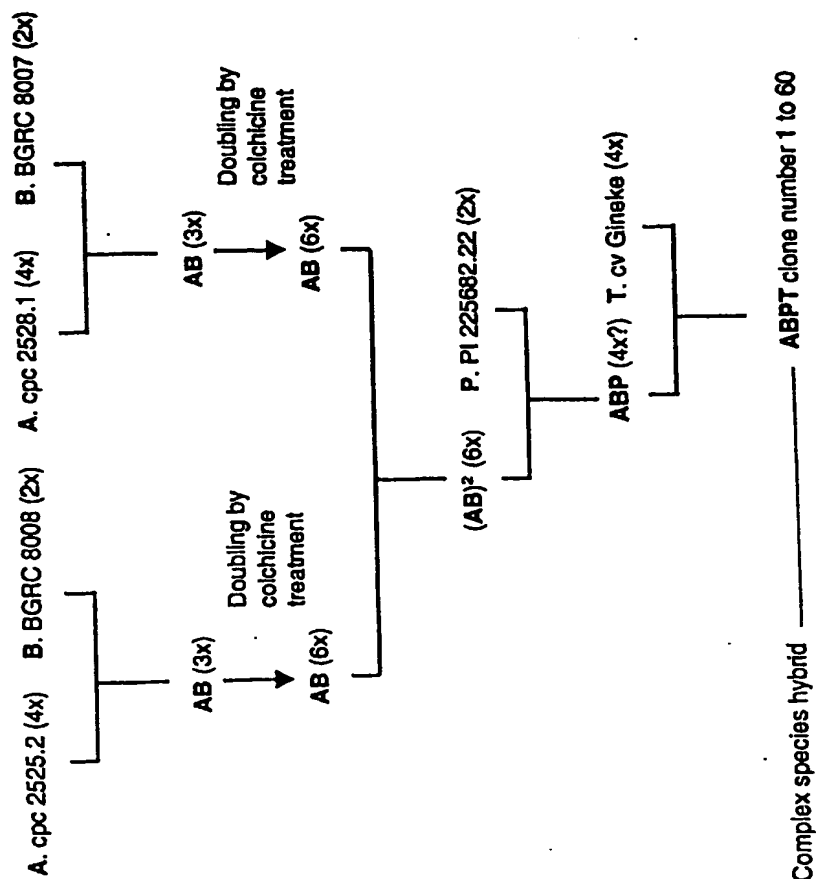


Figure 1A

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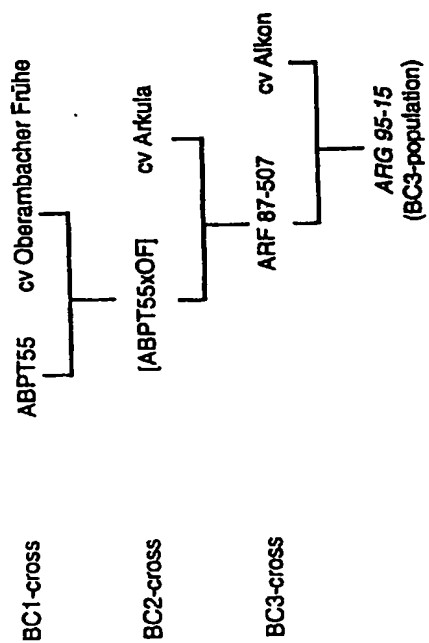


Figure 1B

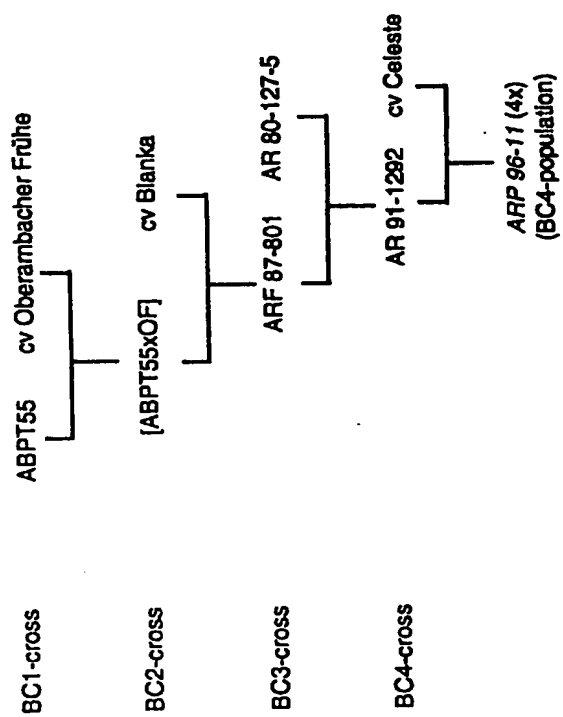


Figure 1C

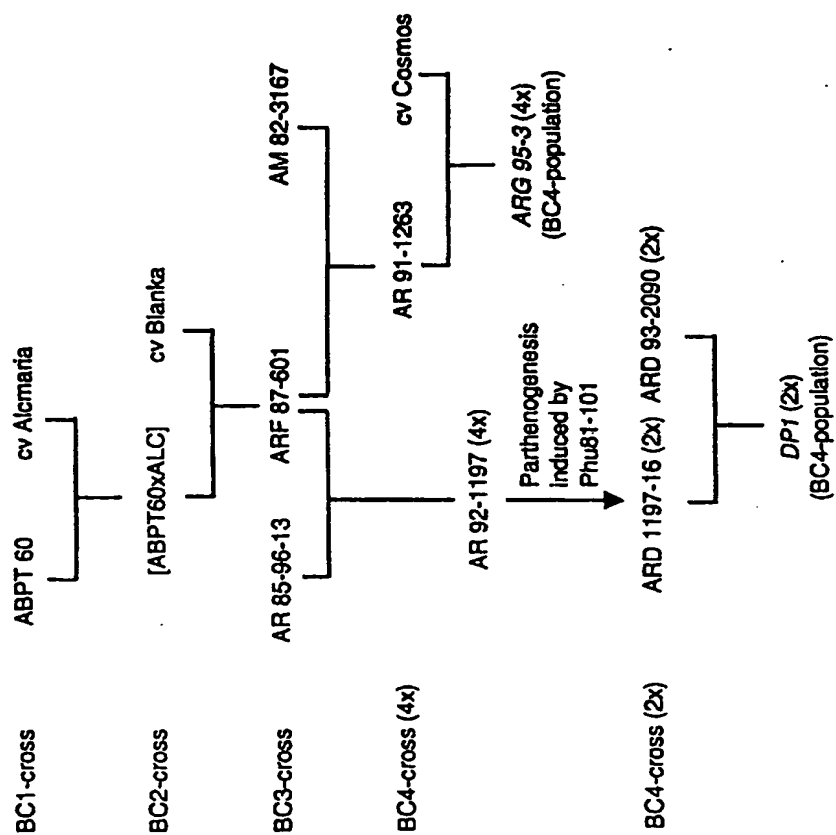


Figure 1D

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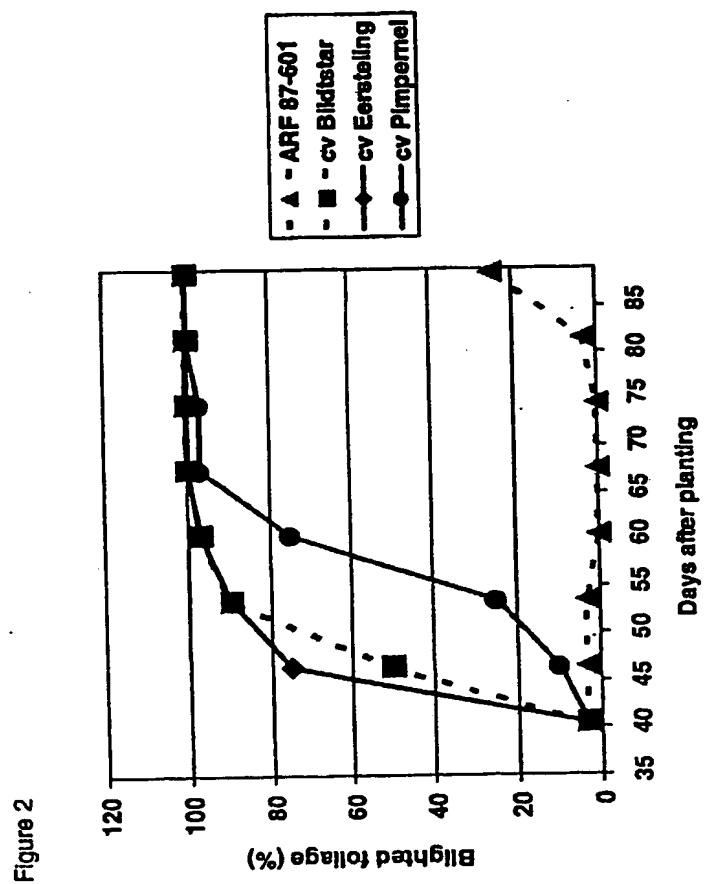


Figure 3

* ARF 87-507 and ARF 87-601 had identical disease progress curves

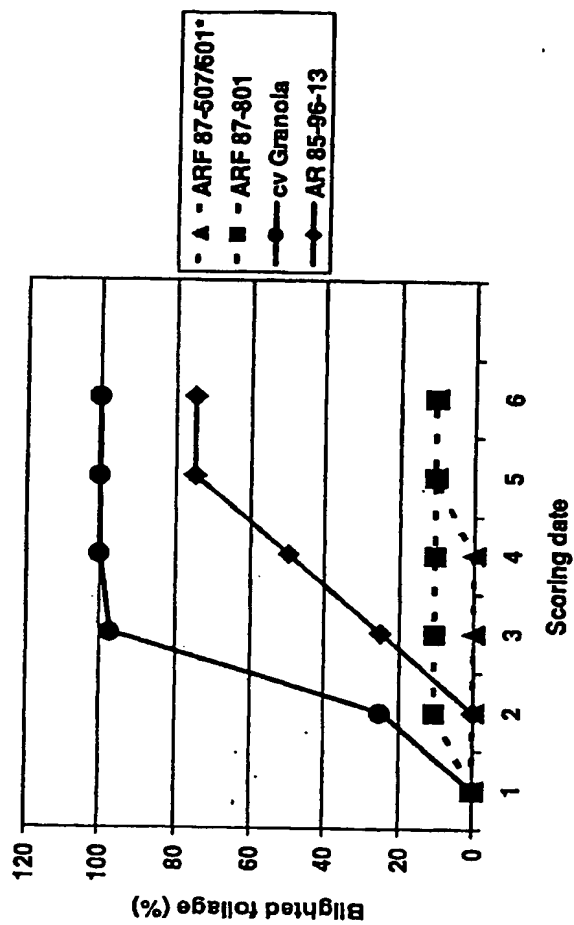




Figure 4



Figure 4 dia 3



Figure 4 dia 4

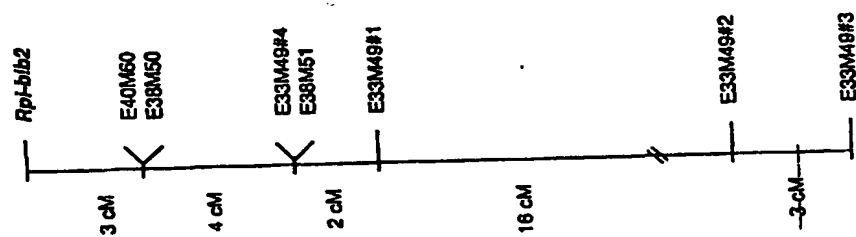


Figure 4 dia 5



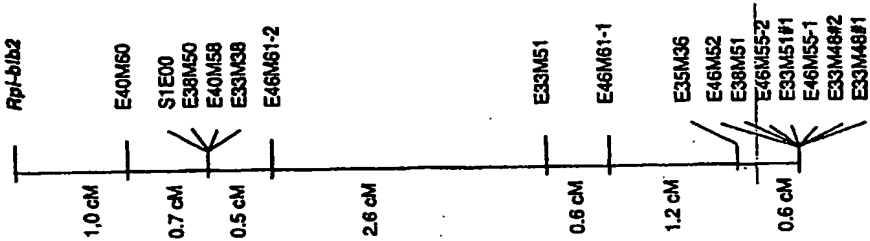
Figure 4 dia 6

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ARG 95-15

Figure 5



ARG 95-3

Figure 6

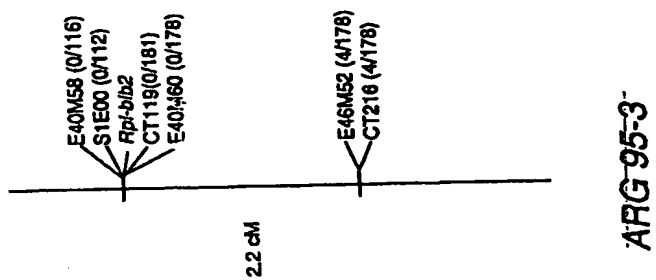


Figure 7

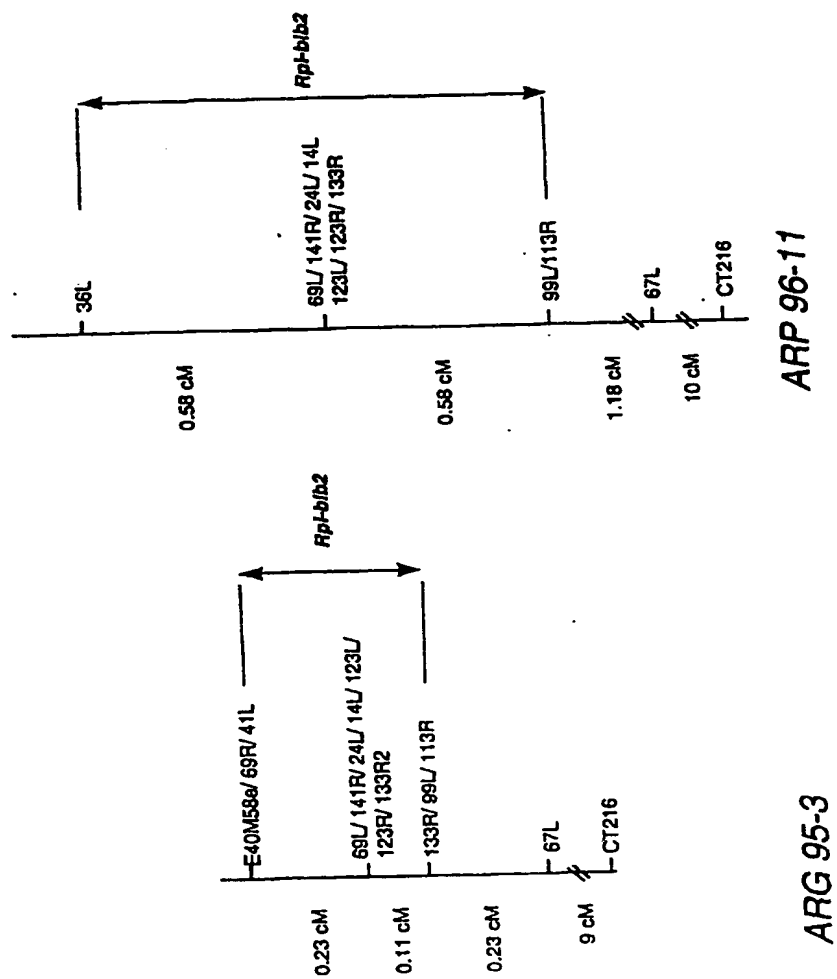


Figure 8

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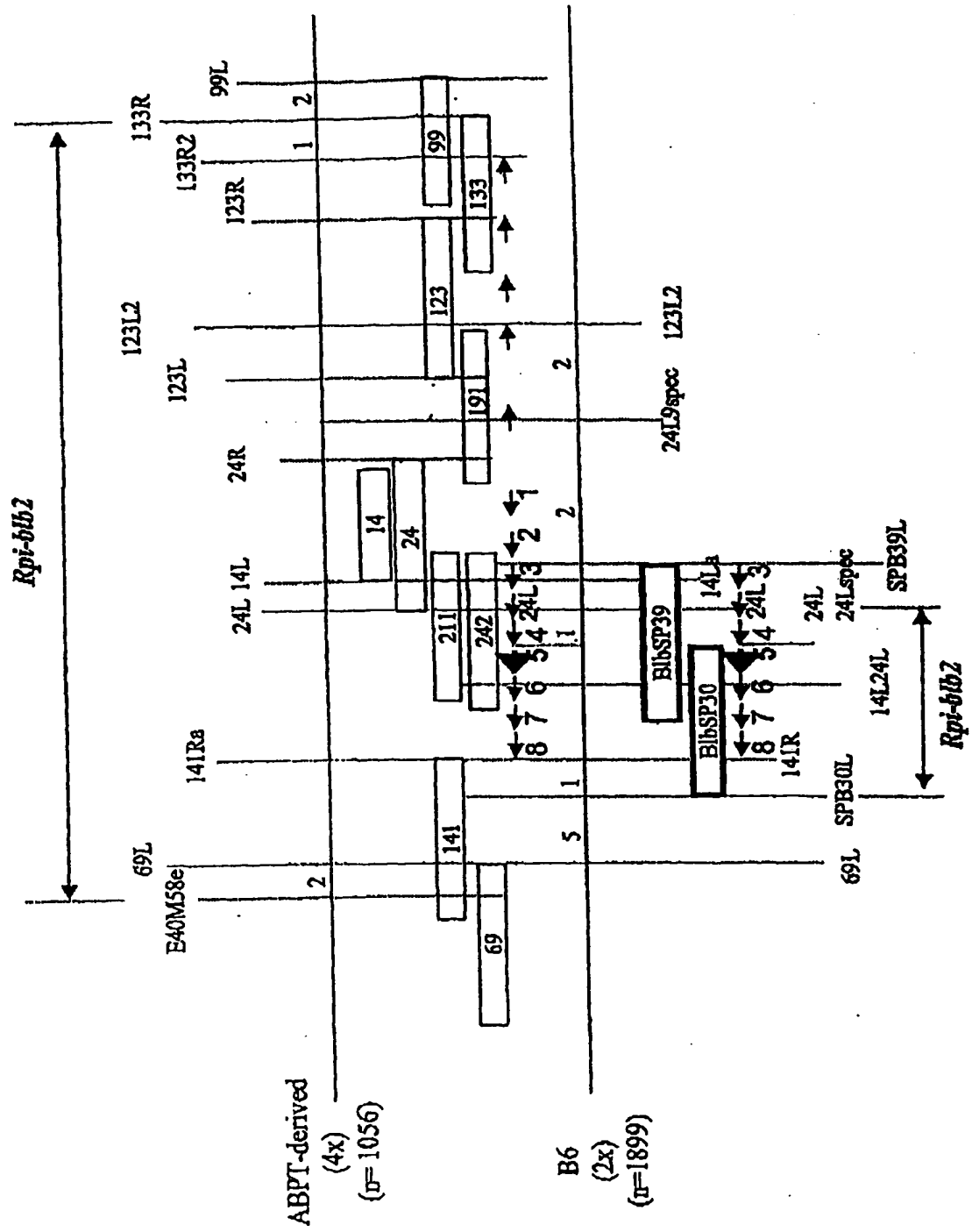


Figure 9

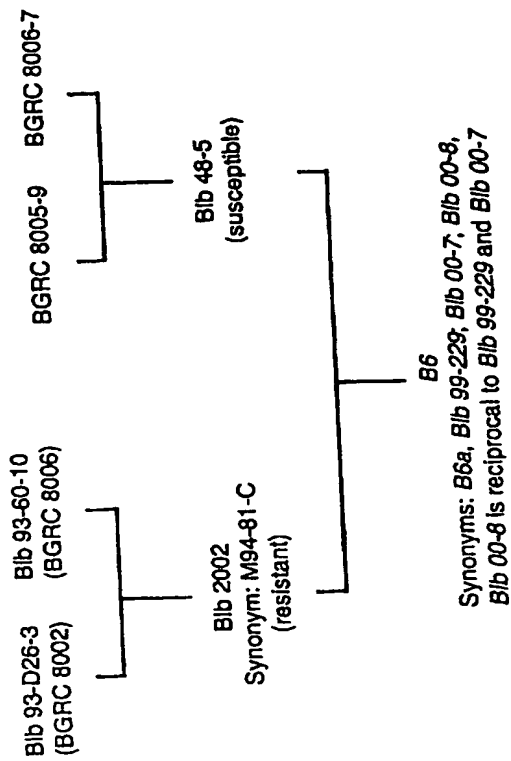


Figure 10

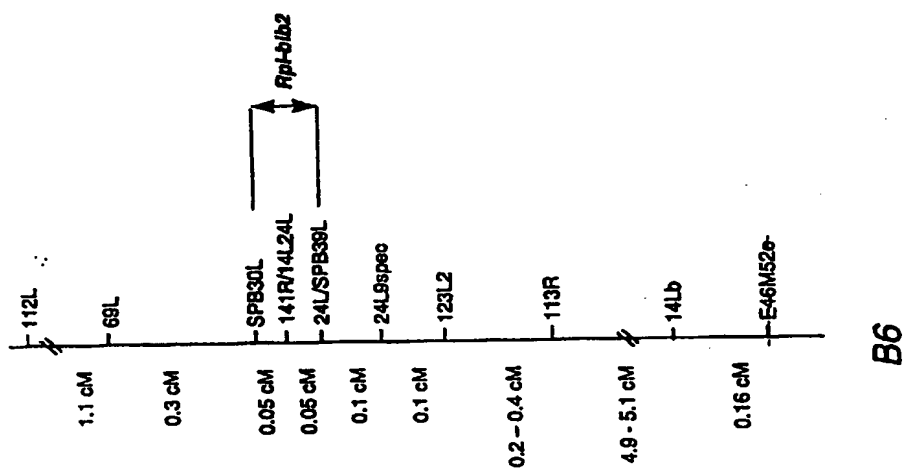


Figure 11

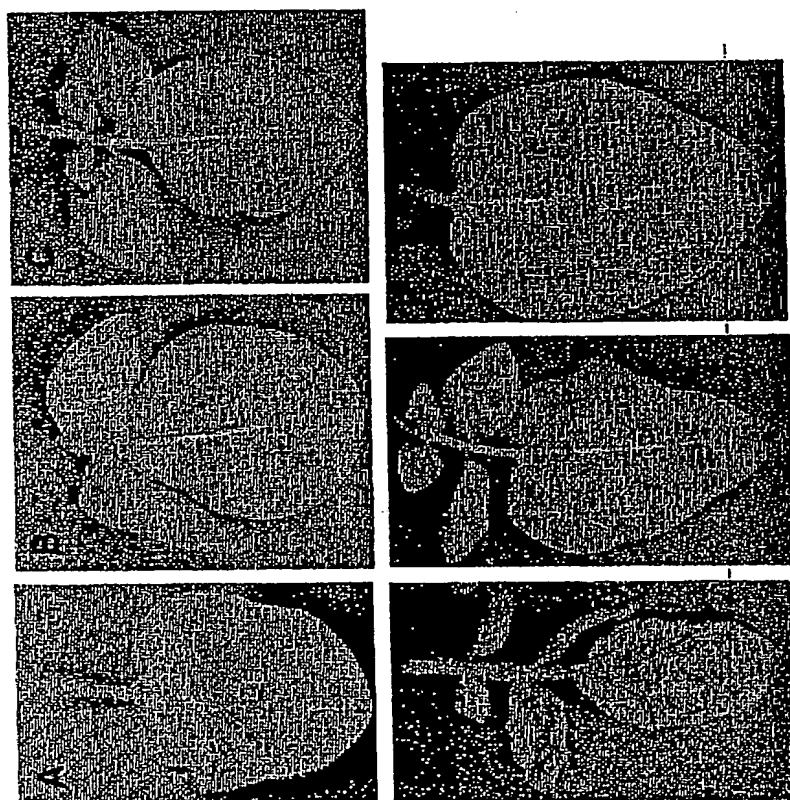


Figure 12

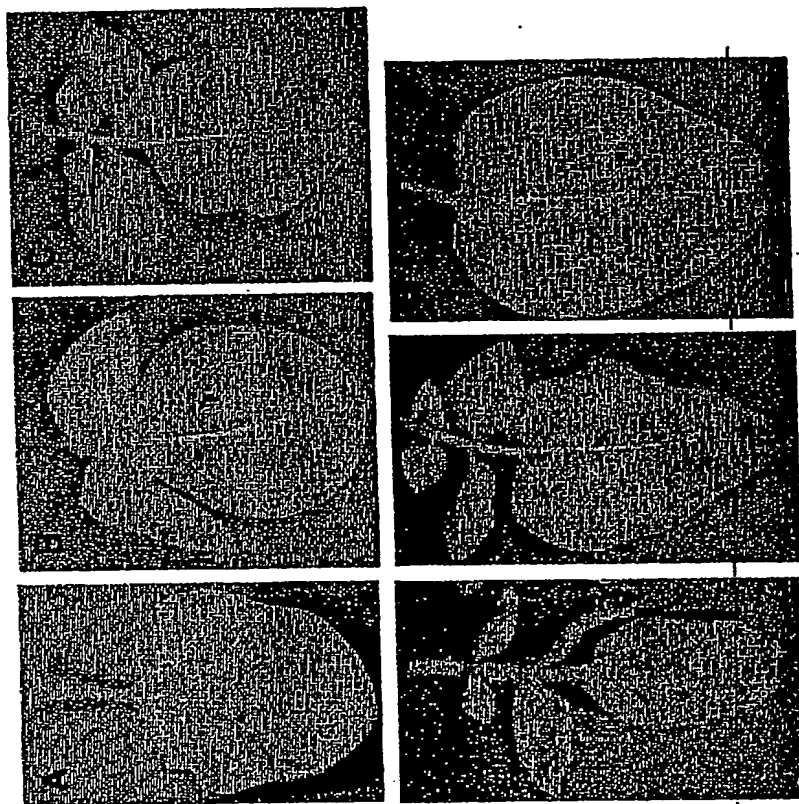


Figure 12 dia2

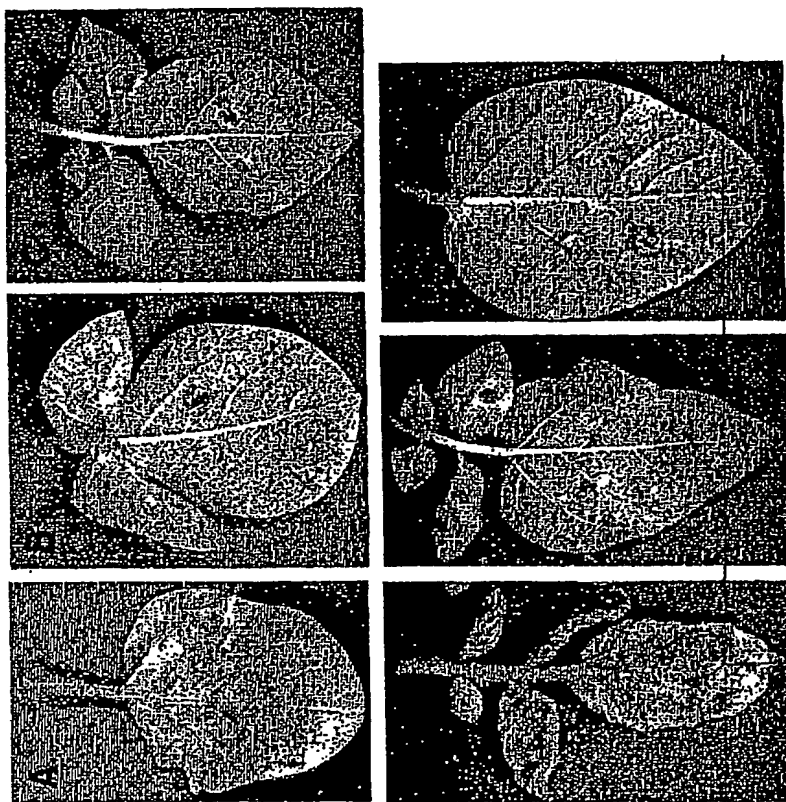


Figure 12 dia 3

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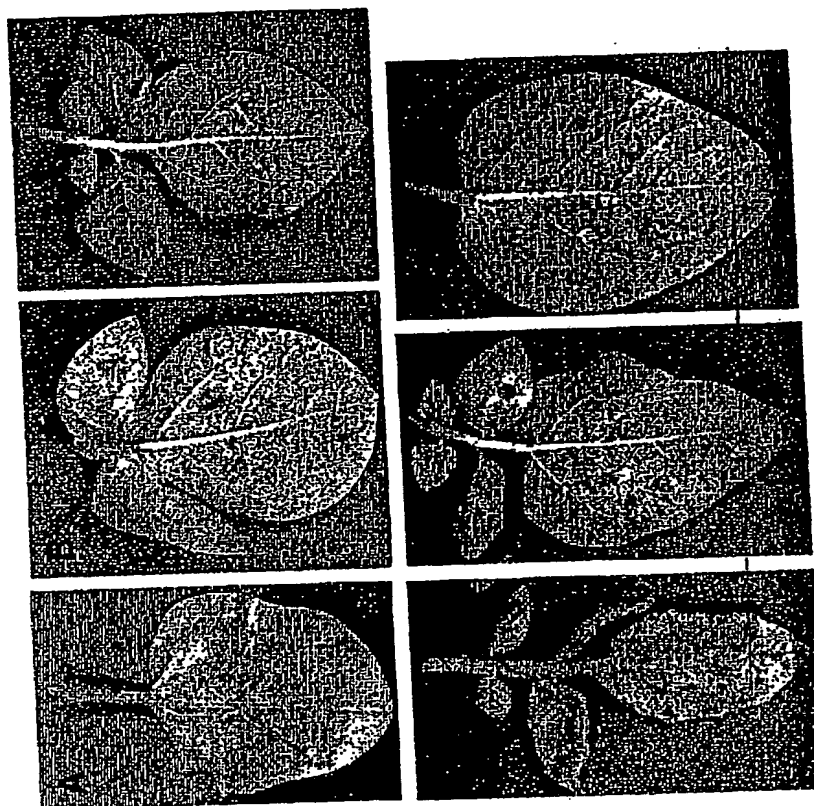


Figure 12 día 4

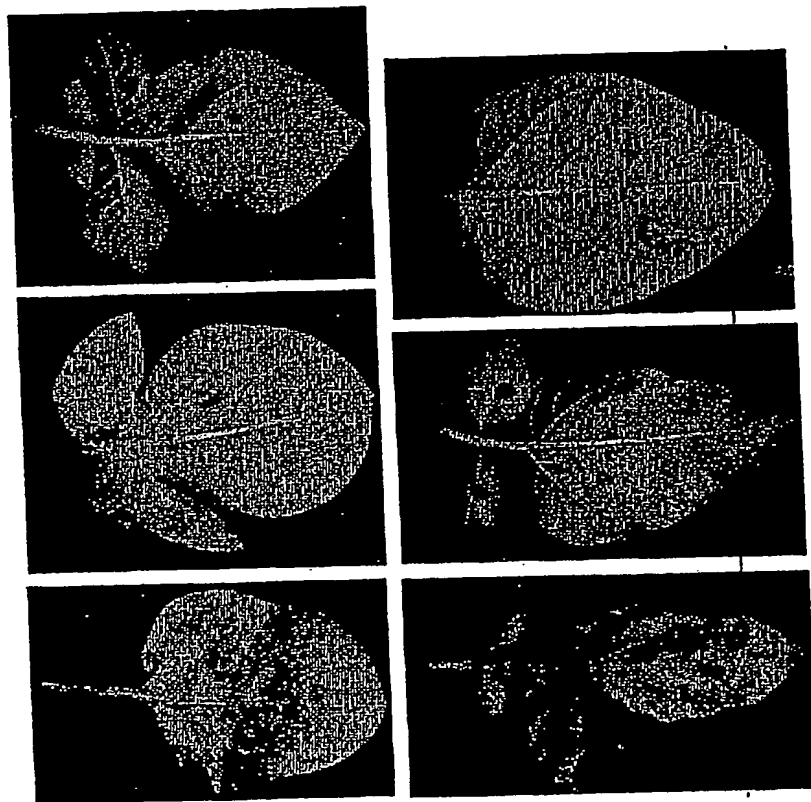


Figure 12 dia 5

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Figure 13A

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Figure 13B

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Figure 13C

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GTTTGTGGATAACAAAGAATCAACCTTGATACTATTACCGAGAATTTGGG 4650
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GGAGGTTGGAGAGGAATCTTTTCCCACGCTTGAGAAATTAGAACTGTCGG 5250
ACTGTCATAATCTTGAGGAGATTCCGCTCTAGTTTTTGGGGATATTTATTCC 5300
TTGAAAATTATCGAACTTGTAAGGAGCCCTCAACTTGAAAATTCCGCTCT 5350
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TTTTAGAAAACTCAGAAGTTTTTAACAAAAATTATAGTTTTTATAAATAC 5600
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CAGGTGGCAACTTTAAATTCATAAAGTATAGGATTGATGACAAACTCGAA 6650
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GCATATGGTTAGTGTGGCTAGAGCAGACAGGATGTATTACCTGGATATCT 6800
ACCAAGACGAATCCACAATCAGTTTTATGTCAAGCAATACATGAAGTAAC 6850
TCCCGATAGAACAGTAAAAGCAAGATGTGTAGGTGTATCTCGACTCTAAG 6900

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TATGAAAAACAAGAAACATCAGGAATGTCCCGTAAACAAAGCAGCCTCAT 7250
GCACAAAACATCCAACGTTGGTAGGATTAATGGAGGGATCGCATCCCAGG 7300
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CTATAGGTTACATGGAGACAACCTTTATGGTTGCTCGTAGGCTCCCGTCAA 7400
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CAGGTAGACGTACATATTTACAAAATTGAGTTTCCTATATAATATGGTTT 7550
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AAAAATAGGAAAGATATTTGTAGTGAGAGGTTTGTACTTTTTATGCTGCT 7650
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AAATATTACAAAAACCCTGATAATAAAATACACTAATCTAAGATATTCAC 7850
TGCAACATACATGCAAAATATATATATATAAAATTTTCATGAAAATTATAA 7900
CAAATAATAGATGTGAACATATAACTTTAAAAATAATATTACATCCATAA 7950
AGCTTAAATTCTAGATC 7967

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Figure 13D

GATCTGCTTCAAATGCTCTGATACCATGTAATTTTCAGTGAATTCTAACTA 50
AACAATGGAGAGAATTAACATATTTTAGAAAGACTGATTGAAGGAGAAGAA 100
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CATTTTCTGTAGTGCCTGCTGAGTGCATTTAACTAACTGCTTAAACATAAA 300
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TCATATTTGGTCTTAATTATTCCTCTGTTTATTTCCAGAATTTTGAGCTC 700
TATACATCTAATAACAAAGCAAGCAGAGGATATATAGTTTCATCAACTAA 750
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AGGTTAGTTGGATCTAACAAGAGAAAGGGAAATAAATTGCAGGAGAAAG 900
AGAGAGGTTAAATACTTACTCACACCACCGATTTACAACAAATCACTTAA 950
TTGTGGTTAGTTAATGTATACCTTCACCTCATTAATTTATTACTTACCCA 1000
TGATAAGTTGTATTAATTTGGTATTAATATCCGGTGCGGGTGAATTCTTA 1005
CCGGGTGAGAGGGATGGGGTTGGAGAGTGTGGAGTGAACAGAAGCAGATG 1100
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TATTACTATACGCTATTAGAGATAGAAAGGTTCCGTACCAGTTGGTCTCG 1200
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CTGCTCTTCGCAAGGATGCTGCCAATGTTCTGGATTTCCCTAGAGAGATTA 1600
AAGAATGAAGAAGATCAAAAGGCTGTTGATGTGGATCTGATTGAAAGCCT 1650

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ATTTGGAGAAGTTTGAAGATATAATGACTAGAAAAAGACAAGAGGTTGAG 1750
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ATATGTCCTTACTAGCCTCGCCGGTAATATGGATGACTGTATAAGCTTGT 1850
ATCATCGTTCTAAATCAGATGCCACCATGATGGATGAGCAATTGGGCTTC 1900
CTCCTCTTGAATCTCTCTCATCTATCCAAGCATCGTGCTGAAAAGATGTT 1950
TCCTGGAGTGACTCAATATGAGGTTCTTCAGAATGTATGTGGCAACATAA 2000
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TACTTTGCAAGTGCGCCGAAGGACTGGGTAAACGACAATCCATGAGTTGAA 3900
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GGATGACCCCTCTCGTCTATAACTTCAACATTAAGCCCTGGCAACTTCTG 6050
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GGGATCGCATTGTCTCCAGCTTTGCAGCATTAGCCAACAGAGCCTCATCG 6150
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AATTAAATTAAATATTTGGAGGTTATGAATATAAAAAGTATCAGAGTTCT 8600
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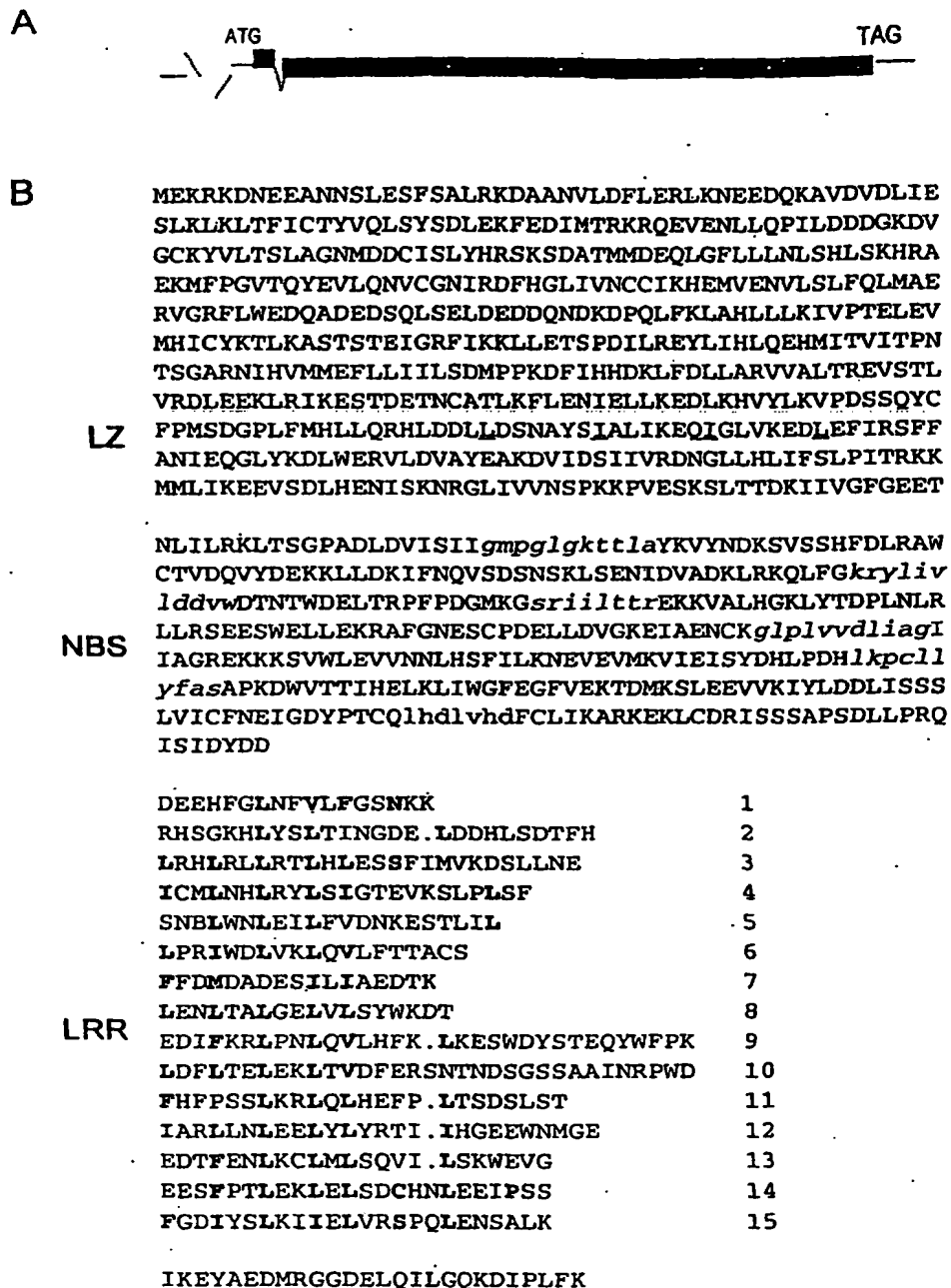


FIGURE 14

PF 54801

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Mi1.1          VL  S  I  D  V  ---  N  L  K  QV  KI  MA
57
Mi1.2          I    VL  S  I  I  ---  N  L  K  QV  KL  MA
57
Rpi-blb2       MEKRKDNEEANNSSLESFSALRKDAANVLDFLERLKNEEDQKAVDVDLIESLKLKLTFFICT
60
Mi1.1          C  F  Q          L  -----  F  TS
109
Mi1.2          Y  F  Q          N    SL  -----  TS
109
Rpi-blb2       YVQLSYSDLKFEFEDIMTRKRQEVENLLQPILDDDGKDVGCKYVLTSLAGNMDDCISLYHR
120
Mi1.1          Y  I    D    Y  H  I          I          G
169
Mi1.2          Y  I    D    Y  H  I          L  G
169
Rpi-blb2       S-KSDATMMDEQLGFLLLNLHLKSHRAEKMPFPGVTQYEVLLQNVCGNIRDFHGLIVNCCI
179
Mi1.1          P    D  H  D  T  R          E  R  SR
229
Mi1.2          P    H    T  R          EH  R  SR  Q  T
229 Rpi-blb2    KHEMVENVLSLFLQMAERVGRFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV 239
Mi1.1          V  I    TN    A  V  L  Q          P  V    S
289
Mi1.2          TN    A  V          I  Q    L  P  S  L
289
Rpi-blb2       PTELEVMIHCYKTLKASTSTEIGRFIKKLETSFDILREYLIHLQEHMITVITPNTSGAR
299
Mi1.1          L    -          D  GV          EP  N  GNNQ
348
Mi1.2          L    -          H  GT          N  GNNQ
348
Rpi-blb2       NIHVMMEFLLIILSDMPKDFIHHDKLFDLLARVVALTREVSTLVRDLEEKLRIKESTDE
359
Mi1.1          DL    K    AL  C          HI  N
408
Mi1.2          DL    K    A  N  C          HM  N
408
Rpi-blb2       TNCATLKFLENIELLKEDLKHVYLKVPDSSQYCFPMSDGPLFMHLLQRLHLLDLSNAYS
419
Mi1.1          E  E  Q  K    VD-A    A
467
Mi1.2          S  E  E  SQE    GDAA    I  A
468
Rpi-blb2       IALIKEQIGLVKEDLEFIRSFAN-IEQGLYKDLWERVLDVAYEAKDVIDSIIVRDNGLL
478
Mi1.1          I  IK    I  A  D  P  D          R    T  E
527
Mi1.2          I  IK    I  A  D  P  D          R    I  E
528
Rpi-blb2       HLIFSLPITRKQMLIKEEVSDLHENISKNRGLIVVNSPKKPVESKSLTTDKIIVGFGE
538
Mi1.1          S    T    S          R          GC
587

```

FIGURE 15

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Mil.2		T	S		R		G	D
588								
Rpi-blb2	TNLILRKLTSGPADLDVISII	<i>gmpglgkttlayKVYNDKSVSSHFDLRAWCTVDQVYDEK</i>						
598								
Mil.1	NT	S	D			T		ESK
647								
Mil.2	T	S	G	D	N		T	L
648								EAK
Rpi-blb2	KLLDKIFNQVSDSNSKLS	ENIDVADKLRLKQLFGKrylivlddvwdTNTWDELTRPFPDGM						
658								
Mil.1		E		N	D	PD		
707								
Mil.2		E		N	D	PD	D	T
708								
Rpi-blb2	KGSRIILT	TREKKVALHGKLYTDPLNLRLLRSEESWELLEKRAFGNESCDELDDVGKEI						
718								
Mil.1		A	V		R	QSS	S	NS
767								L
Mil.2		A	V		R	QSS	S	NS
768								L
Rpi-blb2	AENCKglplvvdliagi	IAGREKKKSVWLEVVNNLHSFILKNEVEVMKVIEISYDHLDPH						
778								
Mil.1		F	TSL	Y	NVYF	A	G	ENM
827								M
Mil.2		H	W	TPL	YLFTVYL	A	E	GI
828								M
Rpi-blb2	1kpcllyfas	APKDWWTTIHKLKLIWGFEGFVEKTDMKSLLEEVVKIYLLDDLISSSLVICF						
838								
Mil.1		YALNF	I		N	F	Q	R
886								T
Mil.2		ILNF	I		N	F	R	
888								T
Rpi-blb2	NEIGDYPTCQlhd	lvhdFCLIKARKEKLCDRISSSAPSDLLPRQISIDYDDDEEHFGLNE						
898								LRR
Mil.1	M	D		R	I	Q	SV	A
946								V
Mil.2	M	D		R	Q	SV	A	I
948								V
Rpi-blb2	VLFGSNKKRHSGKHL	YSLTINGDELDDHLSDTFHLRHLRLRLTLHLESSEFIMVKDSSLNE						
958								
Mil.1		1		2			3	
1006			D	Q	Y	S	STNR	V
Mil.2								L
1008			R	R	Q	Y	F	S
Rpi-blb2								S
1018								G
Mil.1								I
1066								V
Mil.2								D
1068								N
Rpi-blb2								K
1078								E
Mil.1								L
1126								L
Mil.2								L
1128								L

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Rpi-blb2 STEQYWFPKLDFLTELEKLTVD~~FE~~RSNTNDSGSSAAINRPWDFHFPSSLKRLQLHEFPLT
1138

10 11
Mi1.1 P S H F NFN SI
1186

Mi1.2 P N S D Q F N RLLT
1188

Rpi-blb2 SDSLS~~TIARLLNLEELVLYRTI~~IHGEEWNMG~~EEDTFENLKCLML~~SOVILSKWEVGEESFP
1198

12 13
Mi1.1 N K RG K P S KI K D
1246

Mi1.2 N K QE GK P F KI K D K ND
1248

Rpi-blb2 TLEKLELSDCHNLEEIPSSFGDIYSLK~~IELVRS~~POLENSALKIKEYAEDMRGGDELQIL
1258

14 15

Mi1.1 N 1255

Mi1.2 N 1257

Rpi-blb2 GQKDIPLFK 1267

Figure 16: Multiple Sequence Alignments of Mil.1, Mil.2 and Rpi-blb2 nucleic acids

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: Mil.1 3768 bp
 Sequence 2: Mil.2 3774 bp
 Sequence 3: Rpi-blb2 3804 bp
 Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 95
 Sequences (1:3) Aligned. Score: 89
 Sequences (2:3) Aligned. Score: 89

Guide tree file created: [/ebi/externserv/clustalw-work/interactive/clustalw-20040503-14435620.dnd]

Start of Multiple Alignment

There are 2 groups

Aligning...

Group 1: Sequences: 2 Score: 68908
 Group 2: Sequences: 3 Score: 65855

Alignment Score 66872

CLUSTAL-Alignment file created [/ebi/externserv/clustalw-work/interactive/clustalw-20040503-14435620.aln]

CLUSTAL W (1.82) multiple sequence alignment

Figure 17: Multiple Sequence Alignments of Mil.1.1, Mil.2 and Rpi-blb2 proteins

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: Mil.1 1255 aa
 Sequence 2: Mil.2 1257 aa
 Sequence 3: Rpi-blb2 1267 aa
 Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 91
 Sequences (1:3) Aligned. Score: 82
 Sequences (2:3) Aligned. Score: 81

Guide tree file created: [/ebi/externserv/clustalw-work/interactive/clustalw-20040503-14322840.dnd]

Start of Multiple Alignment

There are 2 groups

Aligning...

Group 1: Sequences: 2 Score:25939
 Group 2: Sequences: 3 Score:24668

Alignment Score 19405

CLUSTAL-Alignment file created [/ebi/externserv/clustalw-work/interactive/clustalw-20040503-14322840.aln]

CLUSTAL W (1.82) multiple sequence alignment

Mil.1 MEKRKDNEEANNLSVLFSAISKDIADVLFLE---NEENQKALDKDQVEKIKLKMAFICT 57

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Mi1.2
Rpi-blb2
MEKRKDIEEANNLSVLFSAISKDIANVLIFLE---NEENQKALDKDQVEKCLKMAFICT 57
MEKRKDNEEANNLSLESFSAIRKDAANVLDFLERLKNEEDQKAVDVLIESLKLKLTFTICT 60

YVQLSCSDFEQFEDIMTRKRQEVENLLQPLDDDD-----VFTSLTSNMDDCISLYHR 109
YVQLSYSDFEQFEDIMTRNRQEVENLLQSLDDDD-----VLTSLTSNMDDCISLYHR 109
YVQLSYSDLKFKFEDIMTRKRQEVENLLQPLDDDDGKDVGCKYVLTSLAGNMDDCISLYHR 120

SYKSDAIMMDEQLDFLLNLYHLSKHHAEKIFPGVTQYEVLQNICGNIRDFHGLIVNGCI 169
SYKSDAIMMDEQLDFLLNLYHLSKHHAEKIFPGVTQYEVLQNVCGNIRDFHGLILNGCI 169
S-KSDATMMDEQLGFLLLNLSHLKHHAEKMFPGVTQYEVLQNVCGNIRDFHGLIVNCCI 179

KHEMVENVLPFLQMAERVGHFLLWDDQTDDEDSRLSELDEDEQNDRDSRLFKLAHLLLKIV 229
KHEMVENVLPFLQMAERVGHFLLWEDQTDDEDSRLSELDEDEHNDRDSRLFQLTHLLLKIV 229
KHEMVENVLSLFLQMAERVGREFLWEDQADEDSQLSELDEDDQNDKDPQLFKLAHLLLKIV 239

PVELEVIHICYTNLKASTSAEVGLFIKQLLETSPDILREYLIPLQEHMVTVITPSTSGAR 289
PTELEVMIHICYTNLKASTSAEVGRFIIKQLLETSPDILREYIIQLOEHMTVIPPSTLGR 289
PTELEVMIHICYTKLTKASTSTEIGRFIIKQLLETSPDILREYLHLQEHMITVITPNTSGAR 299

NIHVMMEFLLILSDMP-KDFIHHDKLFDLLDRVGVLTRVSTLVRDLEEEPRNKEGNNQ 348
NIHVMMEFLLILSDMP-KDFIHHDKLFDLLAHVGTLTRVSTLVRDLEEKLRNKEGNNQ 348
NIHVMMEFLLILSDMPKDFIHHDKLFDLLARVVALTRVSTLVRDLEEKLRKESTDE 359

TNCATLDLLENIELKKDLKHVYLKALDSSQCCFPMSDGPFLFMHLHLNDLLDSNAYS 408
TNCATLDLLENIELKKDLKHVYLKAPNSSQCCFPMSDGPFLFMHLHLNDLLDSNAYS 408

SDSLSTIARLPNLEELSLYHTIIHGEWNMGEEDTFENLKFLNFQVSIKWEVGESEFP 1186
SDSLSTIARLPNLENLSLYDTIIQGEWNMGEEDTFENLKFLNRLITLSKWEVGESEFP 1188
SDSLSTIARLLNLEELYLYRTIIHGEWNMGEEDTFENLKCLMLSQVILSKWEVGESEFP 1198
***** * : : *****

Mi1.1
Mi1.2
Rpi-blb2

NLEKLRGCHKLEEI PP SF GDIYSLKSIKIVKSPQLEDSALKIKEYAEDMRGGDELQIL 1246
NLEKLRGCHKLEEI PP SF GDIYSLKFIKIVKSPQLEDSALKIKKYEADMRGGNDLQIL 1248
TLEKLELSDCHNLEEI PP SF GDIYSLKIIELVRSPQLENSALKIKEYAEDMRGGDELQIL 1258
***** * : : *****

Mi1.1
Mi1.2
Rpi-blb2

GQKNIPLEK 1255
GQKNIPLEK 1257
GQKDIPLEK 1267

Mi1.1
Mi1.2
Rpi-blb2

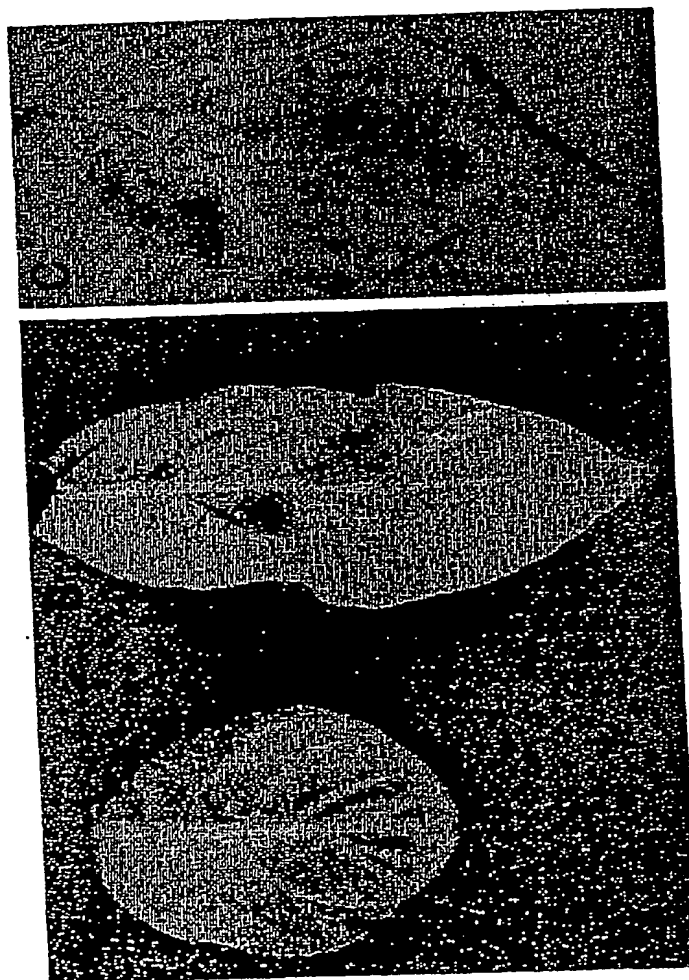


Figure 18

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